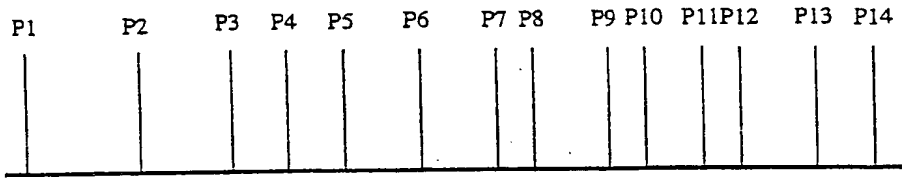
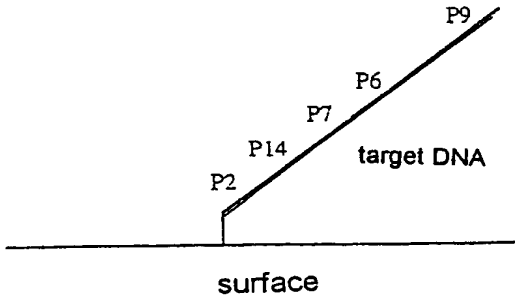
1. Mass distribution of the probes



2. Hybridization



3. Mass distribution of the hybridized probes

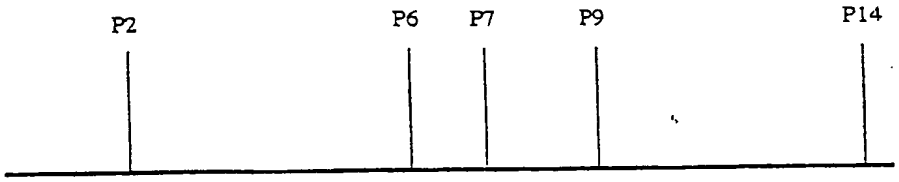
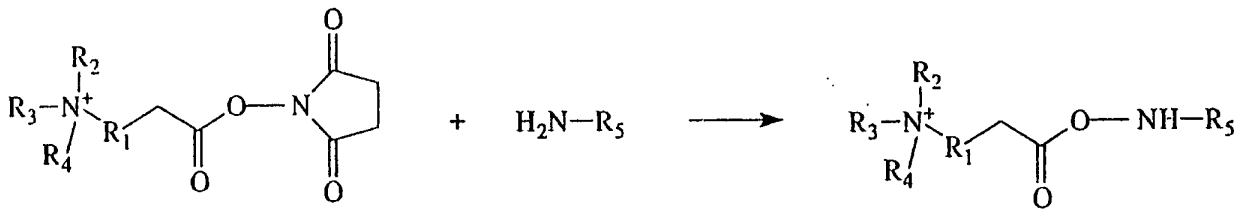


Fig. 1

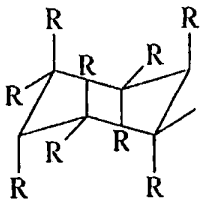
Fig. 2

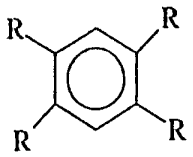
N-terminal mass/charge tagging



R = e.g. alkyl, $-CH_3$, $-C_2H_5$, $-C_3H_7$, $-C_4H_9$ etc.

R_1 = e.g. $(\diagup)_n$

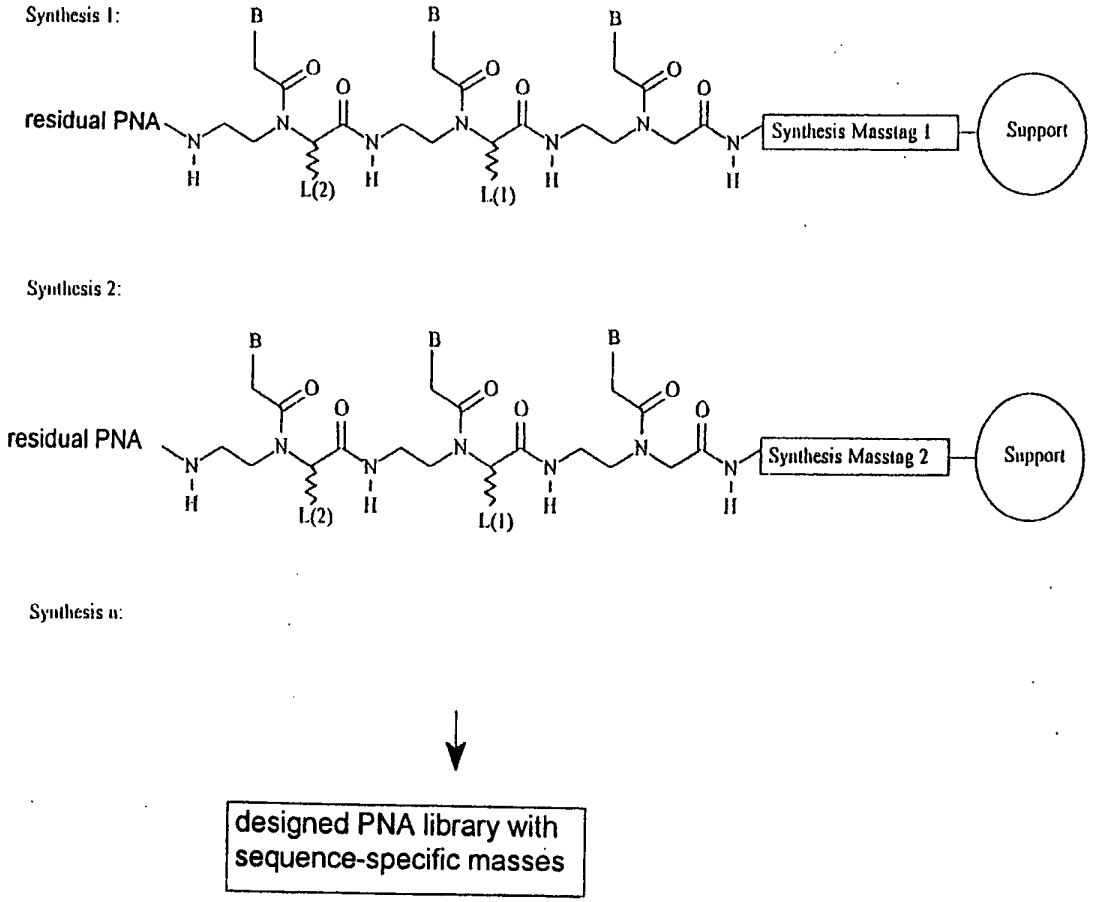




$R_{2\text{-}4}$ = e.g. alkyl, substituted alkyl

R_5 = e.g. nucleic acid, PNA, methyl phosphonate nucleic acid, phosphorothioate nucleic acid

Fig. 3



B = adenine, cytosine, guanine, thymine or purine or pyrimidine derivatives or their deaza analogues

L(n) are various sets of substituents, selected specifically for each base, which are inserted in each synthesis step in order to obtain minimized peak overlaps in the MALDI-MS.

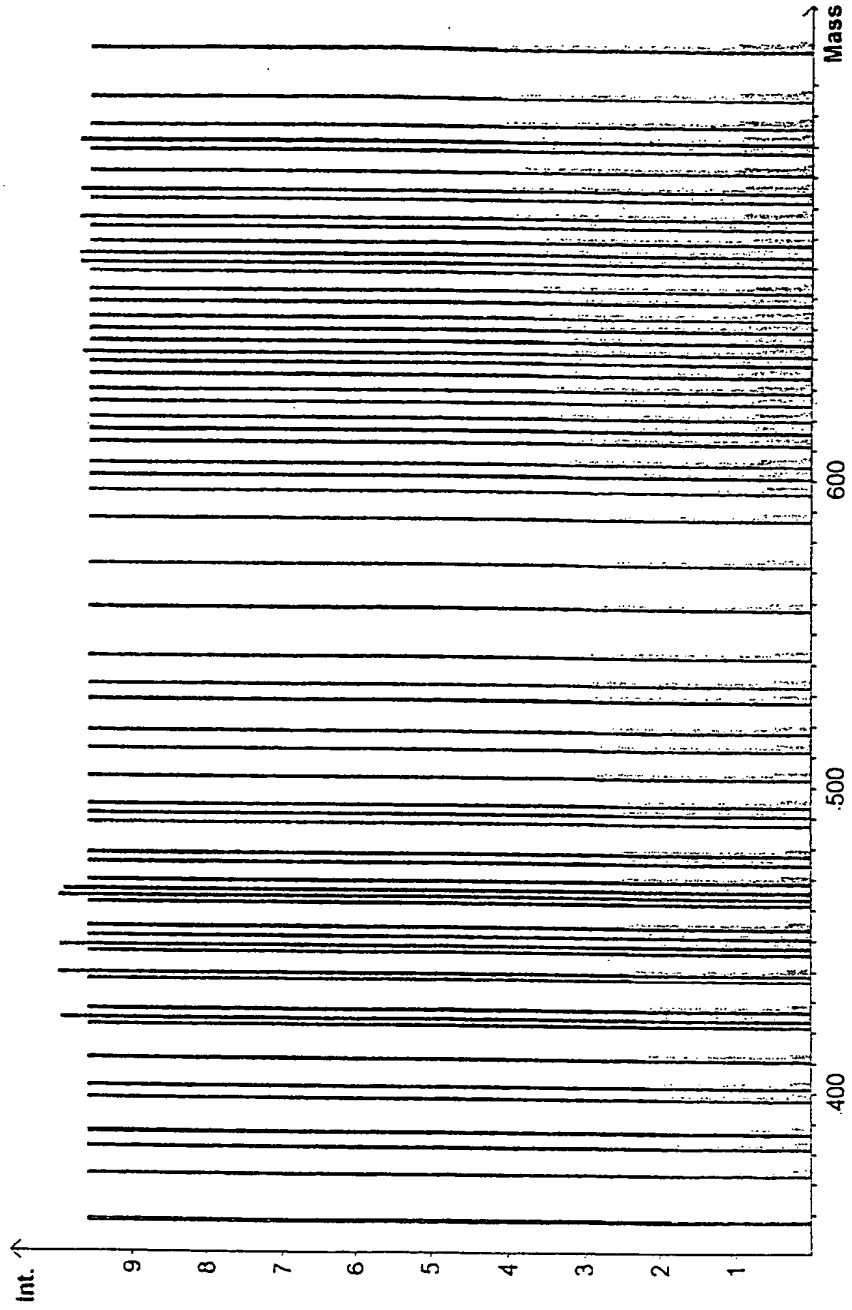


Fig. 4

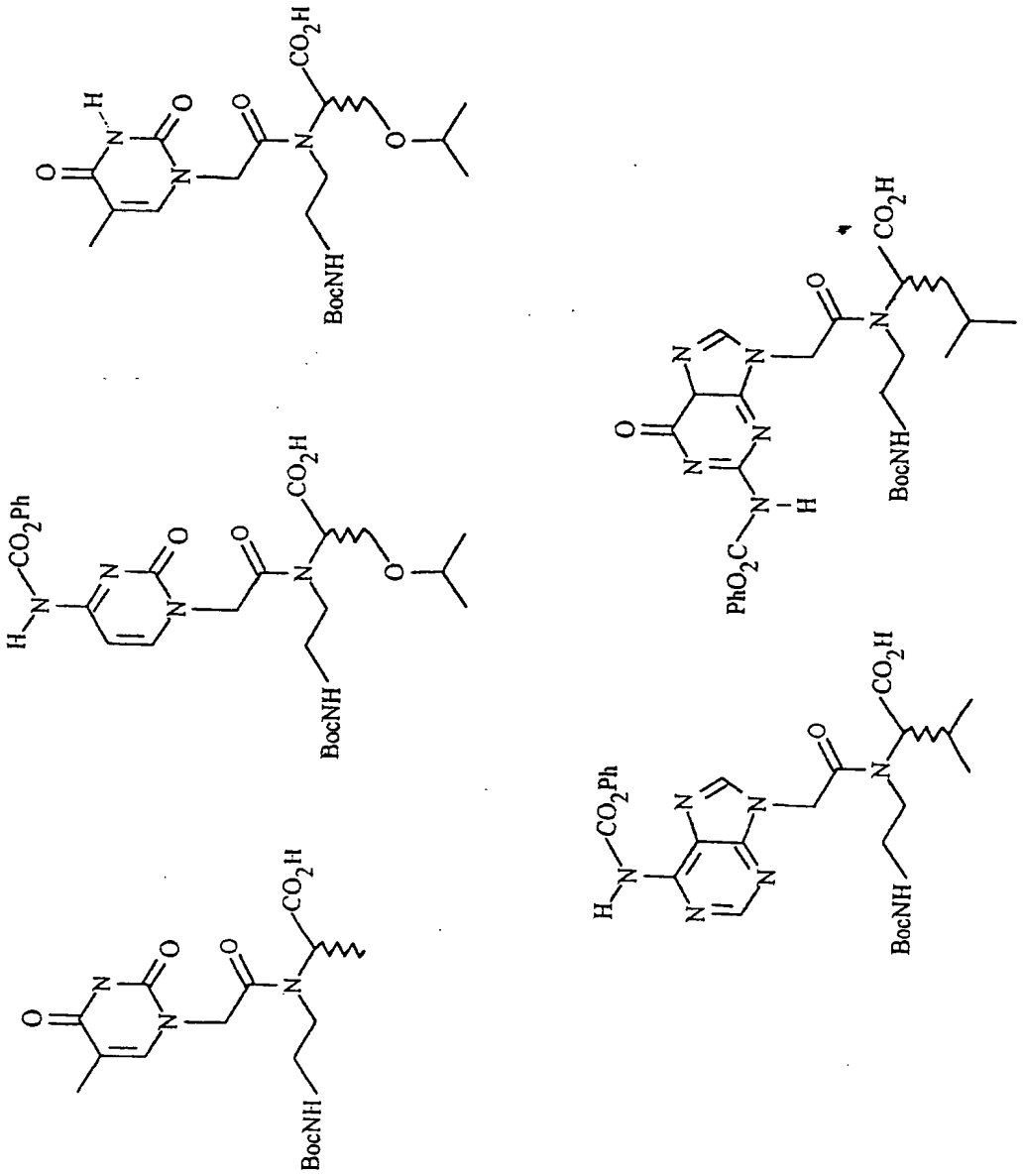


Fig. 5

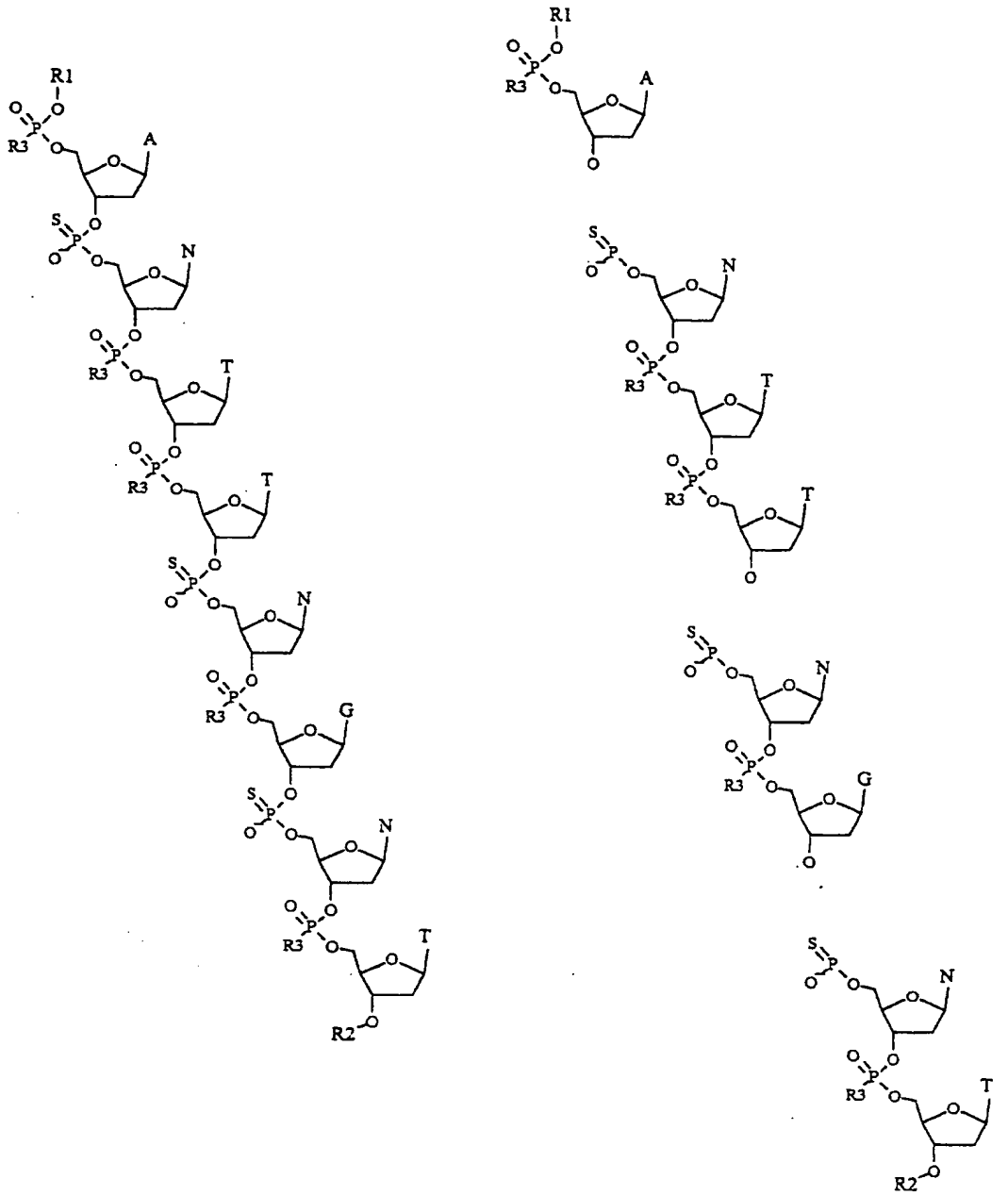


Fig. 6